

Fig. 1

ced-9 genomic 930608 Sequence

10 20 30 40 50 60 70 80 90 100  
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

ClaI  
BspDI  
▼  
ATCGATAGTC GTCACCAAT GGATTTTCG ATTCTCACT AGTCATGGC TCACAATTTA CAAATCTCG AGAAAAGAAA GGATGCAAG AGTATGAAGA 100

SspI DraI BstBI  
▼ ▼ ▼  
GGTCCGAAT CTAAATATTT TAATTTAAAA AATCAATTT CGAATTGAAA TTCAACTCCT ACTCGTTTTC AAAATGCCAA TCCTTTAAGT AAATTTCTGG 200

BstBI  
▼  
ATCGCCCAAT TCTTCCAGAA ATTCTTCAA AGTAGTGGTT TTGTACTGAT TTCTCCGCA AAGAATAGGA ACTTTGGAAT CTCTGGAGC GAAACGGAT 300

SspI  
▼  
TTTSATAACA AAAAATATC CAGACAAAC ATAGACTTTT TTCAAAATTT CTTTATTTGG CTGTCCATTT GGAAGCACC AATCTTTAAC GCTGTCCAGC 400

NcoI  
▼  
CAGAAGTGT CCACTCGCA AGGATAAAG GTCATTTT GAAGCCGAAT TTCTACTAAA TCTCTAGCA TGGAGTCAT GGATCAGAAA TTGAGGAAT 500

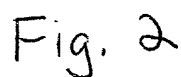
TTTAGATTTC ATCTTGAAAT TTGCAATGGA AAAAATAATT ATTCAAAGAA AATCAGAGAA AATGCAACAA AAAAAACAA AAAAGAACAA AAACAAGTC 600

SraI XbaI EarI Esp3I  
▼ ▼ ▼ ▼  
GAAAAGTGT CCGGGTGT TTGCTGAGC ATCTCTTCAA ACGAGACGC CTGCTGGCG ACTTCTGTG CCTGTGCGT GCATTTCCGC AACAAATTC 700

AACACTTGT TTGAAACGA CCGCCCTGT TCTTTTTC AATTTGATTA GAAATCAGC ATGTTTTCAG GATGATTAAC ATCCCAACTG CGATTTCTGTG 800

1030405060708090100

Fig. 2



Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	\$10,000	\$20,000		
Health status	Good	Fair		
Exercise frequency	Weekly	Monthly		
Stress level	Low	High		
Sleep quality	Good	Poor		
Dietary habits	Healthy	Unhealthy		
Alcohol consumption	None	Occasional		
Tobacco use	Non-smoker	Smoker		
Family size	2	3		
Work hours	40	50		
Commuting time	30	45		
Home ownership	Renter	Owner		
Neighborhood safety	Safe	Unsafe		
Access to green spaces	Yes	No		
Proximity to public transit	Close	Far		
Quality of local schools	High	Low		
Availability of healthcare	Yes	No		
Community engagement	Active	Passive		
Perceived social support	High	Low		
Life satisfaction	High	Low		
Overall well-being	Good	Fair		

ced-9 genomic 930608 Sequence

10	20	30	40	50	60	70	80	90	100	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
TTTTCATCCC GGATTGTAAT TTTTITGTT GATAAATTAG CAGAAAACCTT TACGAATTCG ATTAAAAACG TTATTTTCTA TTCGAATATT TTTAAAGCAT										2500
ATTTTCCTTG APTTGTATT GCGAAAAAGA TCTGCTGATT TATCAAAAAT CGGTTTTTAA ATGTAAAAIT TGTGGAAAAT ACATTAAAAAT TCGATTTTTTG										2600
AACTTTTTTC TTCGAAAAAC AGGTTTTTCT GCIGATTTGC TGAACGAAAA ACCCCAAAAA TTCAATTTTC GAACATTAAA AACCAGAAAA ATCGTTTTTTT										2700
TAAGCTTAAT TTTCGCCAG AATGAACGA ATTAAATTGC AATTTCTAA TTTTCAGATA GGTCATATCT CGTTCCGCCG TTTCGTAGCT GCAAAAATGA										2800
TGAATCCGT GGAACGCGAG GGACAAGTGC GAAACCTCTT CGTTTACACA TCGCTGTTCA TCAAAACGCG GATCCGCAAC AACTGGAAGG AACACAATCG										2900
GAGCTGGTA AGGAGTATTT GCATAGACAT TAGAAGTCAA TATCCCCCTT TCCTAGTAC CCTTGACTTC CCGGGGTGTT GGTAAAGCGA TAATTACAGG										3000
GTTCCGTAGC CTCTTGGGG GACAGCTGA AACATATTCA AGTATATTAC TGTATTATGAT AATGTTATTG TTACGGGAAT ACAAATTCG CAGAATGCTA										3100
TTTCACAACA TATTTGACGC GCAAAATATC CAGTAGAGAA AACTACAGTA ATTCTTTAAA TTTTAAAAAT TTTTACAATT AAAGAAAAATA ACCACTAATC										3200
AAAAGAAATT AATTTCAAAA ATCGAGCCCG TAAATCGACT ACAGTAGGCA TTTTAAAGAT TACTGTAGTT TTCCGTACGA GATATTTCCG CCTCAAATAT										3300

1234567890

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

BsmI  
 GTTGTGAAAT ACGCAATTCAC GGATTTTTGT GTTCCCCGA ATATGCTCTA AAGCATTATT TGTGAAAATA AAAAATCAAG AAAAAAATTG CAGGACGACT 3400

BspHI  
 TCATGACACT CGGAAAACAA ATGAAAGAGG ACTACGAACG AGCAGAAGCT GAAAAAGTGG GACGCCGAA GCAGAACAGA CGGTGGTCGA TGATTGGGCG 3500

PvuII AseI  
 TGGAGTAACA GCTGGAGCCA TTGGAATCGT TGGAGTCGTC GTGTGTGGGC GGATGATGTT CAGCTTGAAG TAACGTATTTC AATTTGTGTA AATAATTAAAT 3600

TTATGTACAA CTCTTACAT TTGAATCTCA TTTTGTCTCA CTGATCTCTT CATCTTTTGA ACTGGAAGAA GTGGGAAAGC TAGGCCACAA ATTACGGCTC 3700

MscI  
 TCTGTGTGCA TTACGATTTT TACTGCAATT TTTTCCGATT GCCTTTTTTT TTGGCCAAAC CCTACTTCGG CGTAATATCA ACTTTTCGGT GTTCTGTACA 3800

EarI  
 TTTCGTCAAA AACCTGAAA CCTAACCTT TCTCGCCGTG GCTAGCCTC CGCTTCTCTT TCACATTTTC CAAAGTACCC CTGTATCTCA ATAATTTCATC 3900

EarI MluI SphI BsiWI  
 TTCACITTA A CTGTCTCTT TCGTGTGGC TCTTCCAAT CCCCCCAAT TCCTGTACGC GTACCGGACT TTGTATTTAT TTTTTCAAA TTGTTTCTC 4000

TCTACACAA CAAAAAAC GGTCTTTTA TTCAACCTT TTTTCGGAAC GAACTGCAA TTTTGATAAT AGCGTGGC AAGAGAATCC GGTTTTCATT 4100

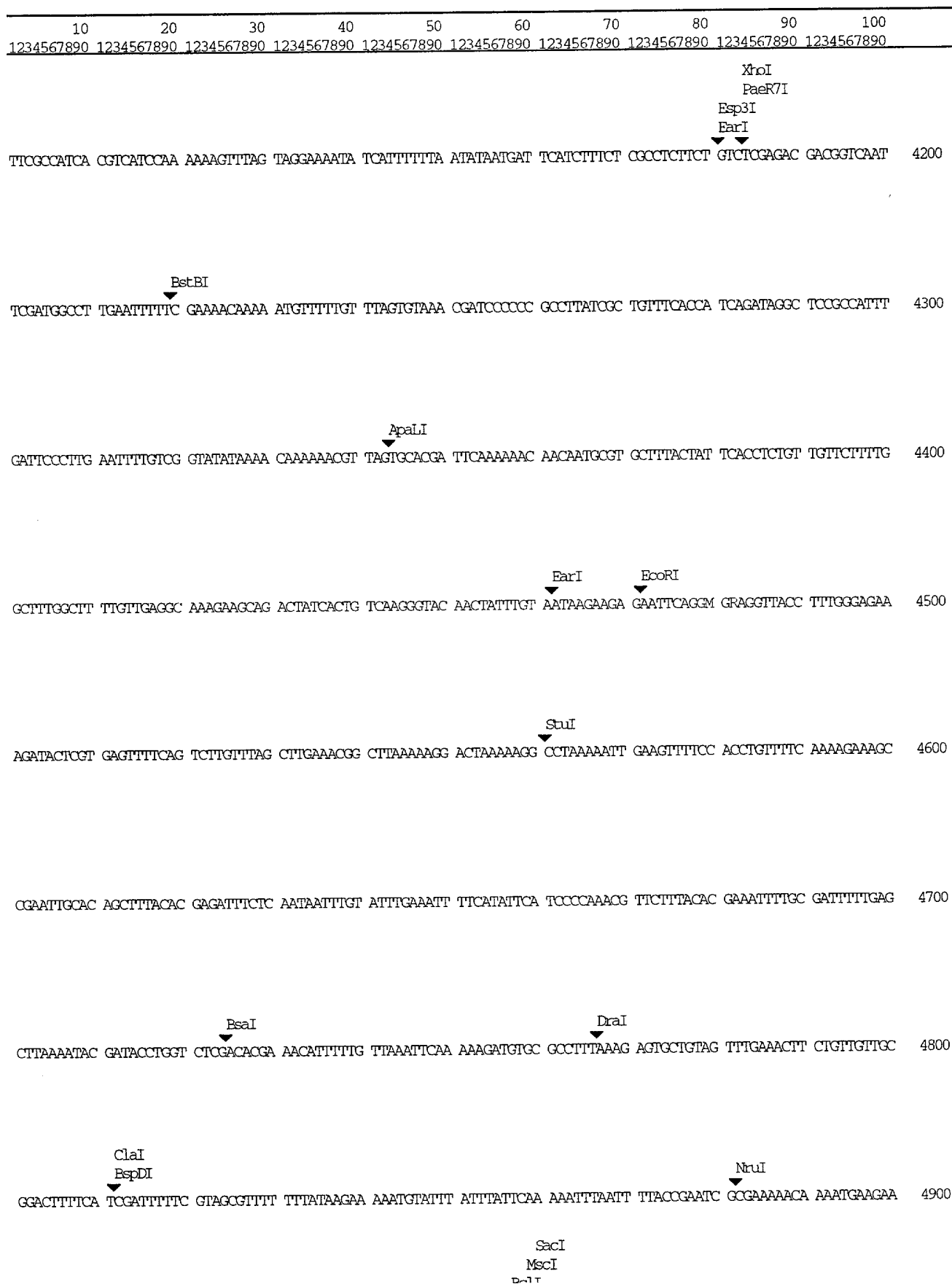


Fig. 2

Fig. 2



10 20 30 40 50 60 70 80 90 100  
 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890  
 CTCTTGATAT TCTTTCCGCT AAAGACAAGG AGAAGTGCTA AGAAAATGTT TTTTTTGTTT GGTTCGCTTG TTTGGAAGGG AAGGACTTTC TATCTCTTTT 5800  
  
 AATTCAACAA TAAACTATTG GAAAACCGTT GAAATTTTAA CCTTGAAC TGAGAAAAGT TCGTGATTA TGTGACAAT TTTGCCAAGT ATATCTTTGT 5900  
  
 EcoRV SspI AseI BstI  
 GGATATCACA ATAAACGAAG TCAAAGCAGC AATATTACG GAAACACAAA ATTAATGAGA ATGCGCAACA TATTGACCG CAAAATATCT CGTAGCGAAA 6000  
  
 Eco47III SacI SspI  
 CTACAGTAAT TCTTCAAAG ACTACTGTAG CGCTGTGTCG AATTACGAGC TCGAATTTTG AATGAATCA GACTAGAAGA AAAGGAGGAA AATATTGAAC 6100  
  
 MniI BbsI  
 ATCAATTGAA CATCAATICA AAAAGTCGAA CCCATGACTA CAGTAGTCTT CTAAAGAATT ACTGTAGTTT TCGCTACGAG ATATTTTGNG NGTCAATAT 6200  
  
 GTTNGCAAT ACGCATCCTC AGAATTGTGT GTTCTCGTAA TGCTTGAAA ATTTTCATT TCAACATCAA ATAAGCAAAT CTAAAAATGT GGGTCTGCA 6300  
  
 PstI DraI  
 GCGACCACTA TGACTGTGAT CGTGGCAAGA CCCACTCAGA AACTACGTC TTCCCTTAAA CAAATACATT TTTAAGTATT GTAGGTATAA AAATTGTGTG 6400  
  
 NheI SalI BbsI HindIII  
 CTACAGTCT AGGCTGCCIT TTTCAGTCA CAACTTCTA ATTTAATCG CGGTCTTCA AAAAGTCGTT TCTTTGAAAA TATAAGCTT TATATATTTA 6500  
  
 EcoRV SpeI  
 TATATTAAAA ATTTTGATTA CATGATATCA AAAGCGACTA GTTTGTATAA AAATTATCAA 6560

10 20 30 40 50 60 70 80 90 100  
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

TTTGAGATGA CACGCTGCAC GCGGACAAAC TCGCTGACGA ATCCGGCGTA TCGGCGACGA ACGATGGCGA CTGGCGAGAT GAAGGACTTT CTGGGGATAA 100  
MetT hrArgCysTh rAlaAspAsn SerLeuThrA snProAlaTy rArgArgArg ThrMetAlaT hrGlyGluMe tLysGluPhe LeuGlylleL

AAGGCACAGA GCCCACCAGT TTTGGAATCA ATAGTGATGC TCAGGACTTG CCATCACCGA GTAGGCAGGC TTCGACGCGA AGAATGTCCA TCGGAGAGTC 200  
ysGlyThrGl uProThrAsp PheGlyIleA snSerAspAl aGlnAspLeu ProSerProS erArgGlnAl aSerThrArg ArgMetSerI leGlyGluSe

EcoRV Sali  
AATTGATGGA AAAATCAATG ATTGGGAAGA GCCAAGGCTT GATATCGAGG GATTGTGGT CCACTATTTC ACGCACCGAA TCCGGCAAAA CGGAATGGAA 300  
rIleAspGly LysIleAsnA spTrpGluGl uProArgLeu AspIleGluG lyPheValVa lAspTyrPhe ThrHisArgI leArgGlnAs nGlyMetGlu

TGTTTTGGAG CACCGGGATT GCCGTGTGGA GTGCAACCGG AGCAGCAAAAT GATGCGAGTT ATGGGAACGA TATTCGAGAA GAAGCAGCGG GAAAAATTTG 400  
TrpPheGlyA laProGlyLe uProCysGly ValGlnProG luHisGluMe tMetArgVal MetGlyThri lePheGluLy sLysHisAla GluAsnPheG

PvuII  
AGACCTTCTG TGAGCAGCTG CTCGCAGTGC CCAGAATCTC ATTTTCACTG TATCAGGATG TGGTTCGGAC GGTTCGAAAT GCACAGACAG ATCAATGTCC 500  
luThrPheCy sGluGlnLeu LeuAlaValP roArgIleSe rPheSerLeu TyrGlnAspV alValArgTh rValGlyAsn AlaGlrThra spGlnCysPr

PstI  
AATGTCTTAT GGACGTTTGA TAGGTCTAAT CTCGTTCCGC GGTTCGTAAG CTGCAAAAAAT GATGGAATCC GTGGAATGCG AGGGACAAGT GCGAAACCTC 600  
oMetSerTyr GlyArgLeuI leGlyLeuIl eSerPheGly GlyPheValA laAlaLysMe tMetGluSer ValGluLeuG lnGlyGlnVa lArgAsnLeu

BamHI BspHI  
TTCGTTTACA CATCGCTGTT CATCAAAACG CGGATCCGCA ACAACTGGAA GGAACACAAT CGGAGCTGGG ACGACTTCAT GACACTCGGA AAACAAATGA 700  
PheValTyrT hrSerLeuPh eIleLysThr ArgIleArgA snAsnTrply sGluHisAsn ArgSerTrpA spAspPheMe tThrLeuGly LysGlnMetL

PvuII  
AAGAGGACTA CGAACGAGCA GAAGCTGAAA AAGTGGGACG CCGGAAGCAG AACAGACGGT GGTGATGAT TGGCGCTGGA GTAACAGCTG GAGCCATTGG 800  
ysGluAspTy rGluArgAla GluAlaGluL ysValGlyAr gArgLysGln AsnArgArgT rpSerMetIl eGlyAlaGly ValThrAlaG lyAlaIleGl

AseI  
AATCGTTGGA GTCGCTGTGT GTGGGCGGAT GATGTTCAAG TTGAAGTAAC GTATTCAATT TGTGTAAATA ATTAATTTAT GTACAATCC TTACATTTGA 900  
yIleValGly ValValValC ysGlyArgMe tMetPheSer LeuLys...

ATCTCATTTT KGCTCACTGA TTCTCTCATC CTTTGAACGT GAAGAAGTGG GAAAGCTAGG CCACAAATTA CGGCTCTCTG TGTCGATTTA CGATTTTACT 1000

Bali  
GCAATTTTTT CCGATTGCCT TTTTTTTTGG CCAAACCCCTA CTCGCGCTA ATATCAACTT TTCCGTGTTT TGTACATTTT GTCAAAAACC CTGAAACCCCT 1100

AACTTTTCTC GCCGTGGCCT AGCCTCCCGC TTCTCTTCCA CATTTCCAAA GTACCCCTGT ATCTCAATAA TTCATCTTCA CTTTAACTGT CTCTTTTCTG 1200

SplI MluI  
GTGGCCTCTT CCAACTCCCC CCAAATTCCT GTACGCGTAC GCGACTTTGT ATTTATTTTT TTCAAATTGT TTTCTCTCTA CAACAACAAA AAAAACGGTT 1300

CAAAAAAAAA AAAAA 1315

Fig. 3

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
MTRCTADNSL	TNPAYRRRTM	ATGEMKEFLG	IKGTEPTDFG	INSDAQDLPS	50
PSRQASTRM	SIGESIDGKI	NDWEEPRLDI	EGFVVDYFTH	RIRQNGMEWF	100
GAPGLPCGVQ	PEHEMMRVMG	TTFEKKHAEN	FETFCEQLLA	VPRISFSLYQ	150
DVVRTVGNAQ	TDQCPMSYGR	LIGLISFGGF	VAAKMMESVE	LQGQVRNLFV	200
YTSLFIKTRI	RNNWKEHNRS	WDDFMTLGKQ	MKEDYERAEA	EKVGRRKQNR	250
RWSMIGAGVT	AGAIGIVGVV	VCGRMMFSLK			280

Fig. 4



Gap Weight: 3.000      Average Match: 0.540  
Length Weight: 0.100    Average Mismatch: -0.396

Quality: 89.8      Length: 298  
Ratio: 0.376      Gaps: 11  
Percent Similarity: 47.059    Percent Identity: 23.077

```

1  ...MTRCTADN.....SLTNPAYRRRTMATGEMKEFLGIKGTEPT 37
   .|. . || .|. . . . : .|. . . . :|. . . .
1  MAHAGRTGYDNREIVMKYIHYKLSQRGYEW...DAGDVGAAPPGAAPAPG 47

38 DFGINSDAQDLPSPSRQASTRRMSIGESIDGKINDWEEPRLDIEGFVVDY 87
   |: . . . . |: . . . . :|. . . . .
48 IFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAA..... 81

88 FTHRIRQNGMEWFGAPGLPCGVQPEHEMMRVMGTIFEKKHAKNFETFCEQ 137
   :|:|:|:|. . . . . :|:|:|:|. . . . . :|:|:|:|. . . . .
82 .....AGPALSPVPPVVHLALRQAGDDFSRRYRGDFAEMSSQ 118

138 LLAVPRISFSLYQDVVRTVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMME 187
   ||. . . . :|. . . . :|. . . . :|. . . . :|. . . . :|. . . .
119 LHLTPFTARGRFATVVEELFRD.....GVNWRIVAFFEFGGVMC...VE 160
   conserved residue mutated in n1950 →
188 SV..ELQGQVRNLFVYTSLFIKTRIRNNWKEHNRSWDDFMTL.GKQMKEL 233
   ||| |: . . | |: . . . . :|. . . . :|. . . . :|. . . . :|. . . .
161 SVNREMSPLVDNIALWMTEYLNRL.HTWIQDNGGWDAFVELYGPSMRPL 209

234 .DYERAEAEKVGRRKQNRWWSMIGAGVTAGAIGIVGVVVCGRMMFSLK 280
   |: . . . . :|. . . . :|. . . . :|. . . . :|. . . . :|. . . .
210 FDFSWLSLCTL.....LSLALVGACITLGAY.....LSHK 239

```

Fig. 6

1 GCGCCCGCCC CTCCGCGCCG CCTGCCC GCC CGCCCGCCG GCTCCCGCCC  
51 GCCGCTCTCC GTGGCCCCGC CGCGCTGCCG CCGCCGCCG TGCCAGCGAA  
101 GGTGCCGGGG CTCCGGGCCC TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC  
151 GAACTGCGCG ACGGGAGGTC CGGGAGGCGA CCGTAGTCGC GCCGCCGCGC  
201 AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG GGGTGCGCCG  
251 GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC  
301 ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCTCCCC CACCACCTCC  
351 TTCTCCCCAC CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG  
401 GCACCGGCGG GCCAGGCGCG TCCTGCCTTC ATTTATCCAG CAGCTTTTCG  
451 GAAAATGCAT TTGCTGTTCG GAGTTTAATC AGAAGACGAT TCCTGCCTCC

Fig. 7-1

501 GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT CCTGGGGAGG  
 551 CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT  
 601 GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA  
 651 ATACCGGACT GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA  
 701 AACTCGAGCT CTTGAGATCT CCGGTTGGGA TTCCTGCGGA TTGACATTTT  
 751 TGTGAAGCAG AAGTCTGGGA ATCGATCTGG AAATCCTCCT AATTTTACT  
 801 CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAA TCAGCTATAA  
 851 CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG  
 901 GTTTTACAAA AAGGAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA  
 951 CAAGTAAGTC TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC  
 1001 CTTTGAGATT TTTTACTTAA AGTGCATTCT AGTAAATTTA ATTTCCAGGC  
 1051 AGCTTAATAC ATTGTTTTTA GCCGTGTTAC TTGTAGTGTG TATGCCCTGC  
 1101 TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA CTTATTAGTT  
 1151 TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA  
 1201 CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA  
 1251 TTGAATAAAA AATTTCTGCT GTCTCATGCC AAGAGGGAAA CACCAGAATC  
 1301 AAGTGTTCCG CGTGATTGAA GACACCCCTT CGTCCAAGAA TGCAAAGCAC  
 1351 ATCCAATAAA ATAGCTGGAT TATAACTCCT CTTCTTTCTC TGGGGGCCGT  
 1401 GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT GCTTTTCCTC  
 1451 TGGGAAGGAT GGCGCACGCT GGGAGAACGG GGTACGACAA CCGGGAGATA  
 1501 GTGATGAAGT ACATCCATTA TAAGCTGTCG CAGAGGGGCT ACGAGTGGGA  
 1551 TGCGGGAGAT GTGGGCGCCG CGCCCCCGGG GGCCGCCCCC GCACCGGGCA  
 1601 TCTTCTCCTC CCAGCCCGGG CACACGCCCC ATCCAGCCGC ATCCCGCGAC  
 1651 CCGGTCGCCA GGACCTCGCC GCTGCAGACC CCGGCTGCCC CCGGCGCCGC  
 1701 CGCGGGGCCCT GCGCTCAGCC CGGTGCCACC TGTGGTCCAC CTGGCCCTCC  
 1751 GCCAAGCCGG CGACGACTTC TCCCGCCGCT ACCGCGGCGA CTTGCGCGAG  
 1801 ATGTCCAGCC AGCTGCACCT GACGCCCTTC ACCGCGCGGG GACGCTTTGC  
 1851 CACGGTGGTG GAGGAGCTCT TCAGGGACGG GGTGAACTGG GGGAGGATTG  
 1901 TGGCCTTCTT TGAGTTCGGT GGGGTCATGT GTGTGGAGAG CGTCAACCGG

Fig. 7-2

1951 GAGATGTCGC CCCTGGTGGA CAACATCGCC CTGTGGATGA CTGAGTACCT  
 2001 GAACCGGCAC CTGCACACCT GGATCCAGGA TAACGGAGGC TGGGATGCCT  
 2051 TTGTGGAAC GTACGGCCCC AGCATGCGGC CTCTGTTTGA TTTCTCCTGG  
 2101 CTGTCTCTGA AGACTCTGCT CAGTTTGGCC CTGGTGGGAG CTTGCATCAC  
 2151 CCTGGGTGCC TATCTGAGCC ACAAGTGAAG TCAACATGCC TGCCCCAAAC  
 2201 AAATATGCAA AAGGTTCACT AAAGCAGTAG AAATAATATG CATTGTCAGT  
 2251 GATGTACCAT GAAACAAAGC TGCAGGCTGT TTAAGAAAAA ATAACACACA  
 2301 TATAAACATC ACACACACAG ACAGACACAC ACACACACAA CAATTAACAG  
 2351 TCTTCAGGCA AAACGTCGAA TCAGCTATTT ACTGCCAAAG GGAAATATCA  
 2401 TTTATTTTTT ACATTATTAA GAAAAAAGAT TTATTTATTT AAGACAGTCC  
 2451 CATCAAACT CCGTCTTTGG AAATCCGACC ACTAATTGCC AAACACCGCT  
 2501 TCGTGTGGCT CCACCTGGAT GTTCTGTGCC TGTAACATA GATTTCGCTTT  
 2551 CCATGTTGTT GGCCGGATCA CCATCTGAAG AGCAGACGGA TGGAAAAAGG  
 2601 ACCTGATCAT TGGGGAAGCT GGCTTTCTGG CTGCTGGAGG CTGGGGAGAA  
 2651 GGTGTTTATT CACTTGCATT TCTTTGCCCT GGGGGCGTGA TATTAACAGA  
 2701 GGGAGGGTTC CCGTGGGGGG AAGTCCATGC CTCCCTGGCC TGAAGAAGAG  
 2751 ACTCTTTGCA TATGACTCAC ATGATGCATA CCTGGTGGGA GGAAAAGAGT  
 2801 TGGGAACTTC AGATGGACCT AGTACCCACT GAGATTTCCA CGCCGAAGGA  
 2851 CAGCGATGGG AAAAATGCCC TTAAATCATA GGAAAGTATT TTTTAAAGCT  
 2901 ACCAATTGTG CCGAGAAAAG CATTTTAGCA ATTTATACAA TATCATCCAG  
 2951 TACCTTAAAC CCTGATTGTG TATATTCATA TATTTTGGAT ACGCACCCCC  
 3001 CAACTCCCAA TACTGGCTCT GTCTGAGTAA GAAACAGAAT CCTCTGGAAC  
 3051 TTGAGGAAGT GAACATTTCT GTGACTTCCG ATCAGGAAGG CTAGAGTTAC  
 3101 CCAGAGCATC AGGCCGCCAC AAGTGCCTGC TTTTAGGAGA CCGAAGTCCG  
 3151 CAGAACCTAC CTGTGTCCCA GCTTGGAGGC CTGGTCTTGG AACTGAGCCG  
 3201 GGCCCTCACT GGCCCTCCTCC AGGGATGATC AACAGGGTAG TGTGGTCTCC  
 3251 GAATGTCTGG AAGCTGATGG ATGGAGCTCA GAATTCCACT GTCAAGAAAG  
 3301 AGCAGTAGAG GGGTGTGGCT GGGCCTGTCA CCCTGGGGCC CTCCAGGTAG  
 3351 GCCCGTTTTT ACGTGGAGCA TAGGAGCCAC GACCCTTCTT AAGACATGTA

Fig. 7-3





4851 GGGATTCACA GAGTATTTGA AAAATGTATA TATATTAAGA GGTACAGGGG  
4901 GCTAATTGCT AGCTGGCTGC CTTTGTCTGT GGGGTTTTGT TACCTGGTTT  
4951 TAATAACAGT AAATGTGCCC AGCCTCTTGG CCCCAGAACT GTACAGTATT  
5001 GTGGCTGCAC TTGCTCTAAG AGTAGTTGAT GTTGCATTTT CCTTATTGTT  
5051 AAAACATGT TAGAAGCAAT GAATGTATAT AAAAGC

Fig. 7-5

*egl-1(sd)* ♂ x *ced-9(n1950 dm)* ♀

$$\frac{ced-9(n1950 \text{ dm})}{+} ; \frac{egl-1(sd)}{+} \quad \text{Common: able to lay eggs}$$
$$\frac{ced-9(n1950 \text{ dm } *)}{+ \quad +} ; \frac{egl-1(sd)}{+} \text{ Rare: egg-laying defective}$$

Fig. 8

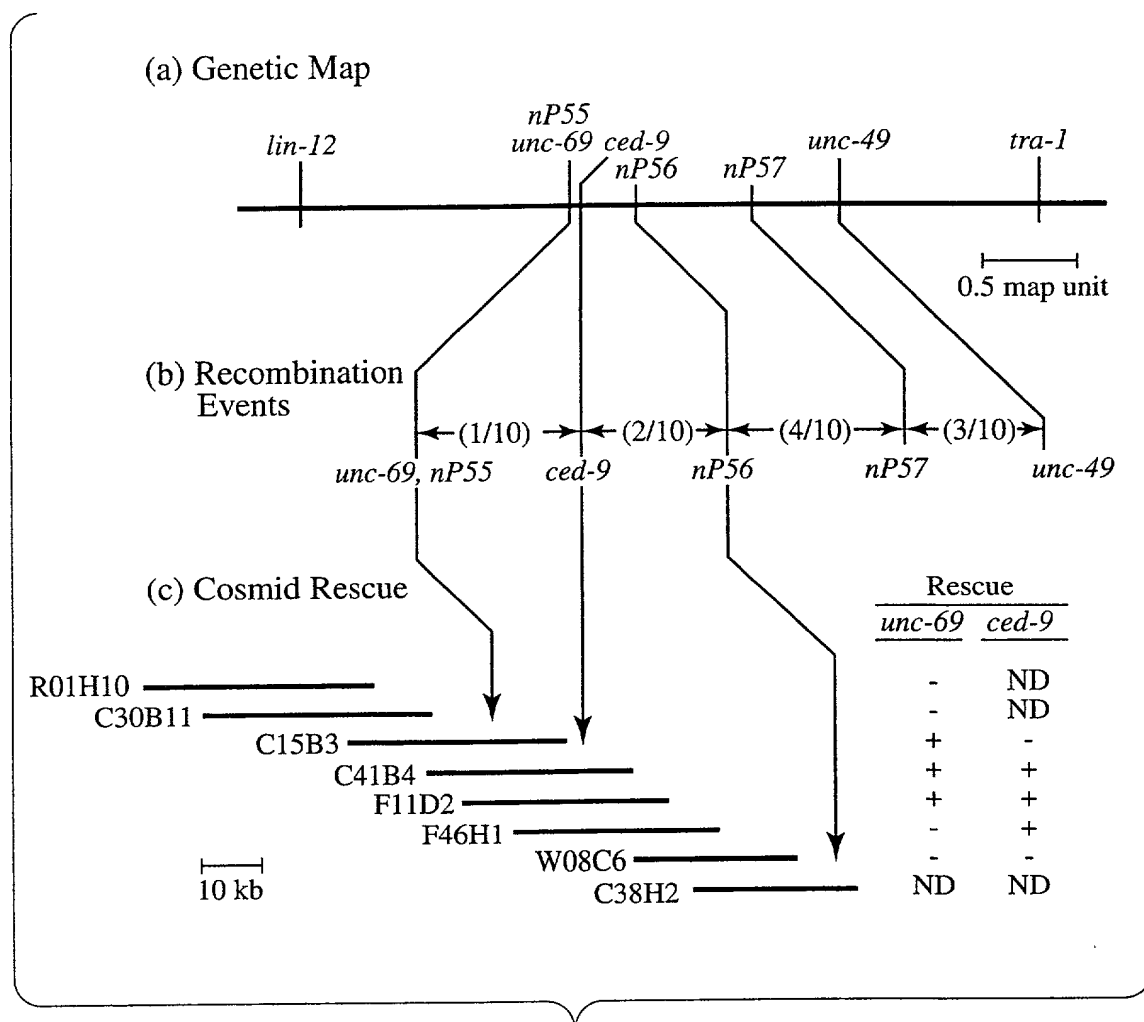


Fig. 9

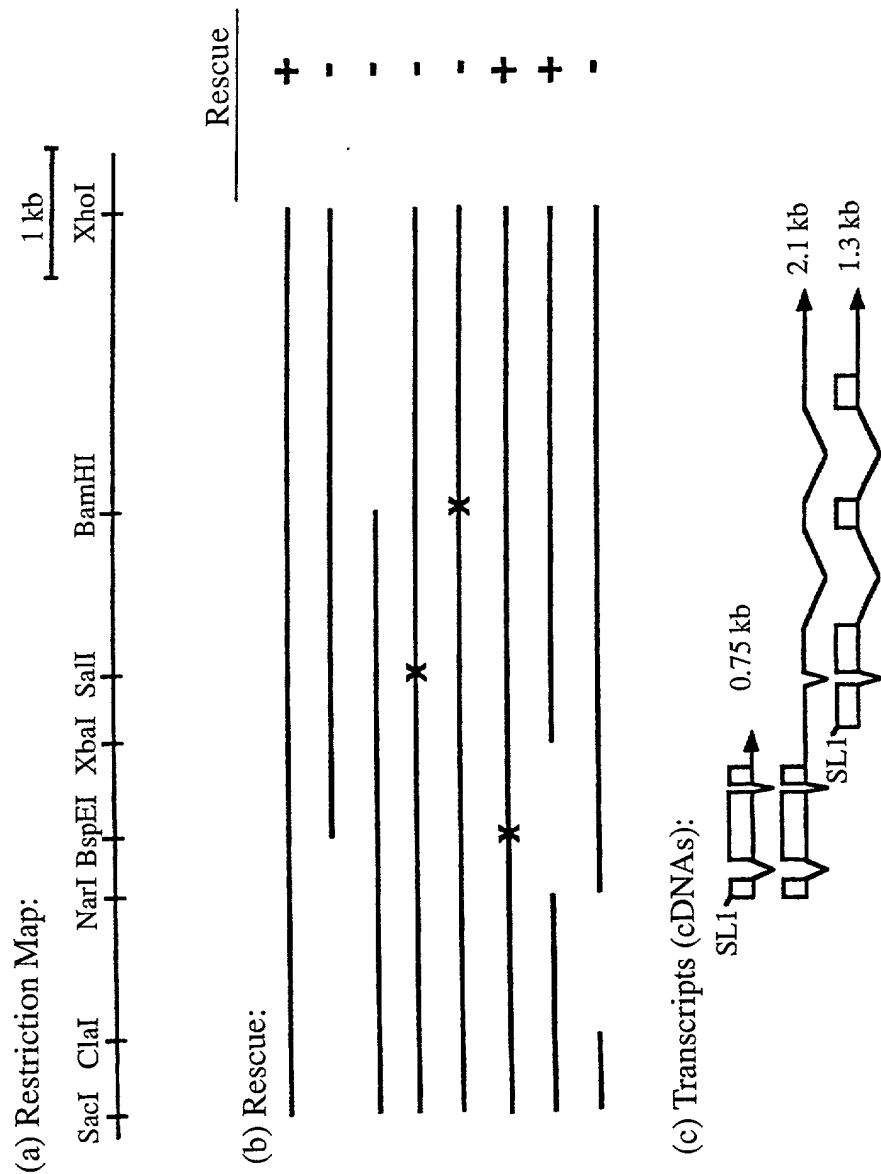


Fig. 10

Figure 11

n3400	
ATG ACA CGC TGC ACG GCG GAC AAC TCG CTG AAT CCG GCG TAT CGG CGA CGA ACG ATG M T R C T A D N S L T N P A Y R R R T M	20
CGC ACT GGC GAG ATG AAG GAG TTT CTG GGG ATA AAA GGC ACA GAG CCC ACC GAT TTT GGA A T G E M K E F L G I K G T E P T D F G	40
ATC AAT AGT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT I N S D A Q D L P S P S R Q A S T R R M	60
TCC ATC GGA GAG TCA ATT GAT GGA AAA ATC AAT GAT TGG GAA GAG CCA AGG CTT GAT ATC S I G E S I D G K I N D W E E P R L D I	80
GAG GGA TTT GTG GTC GAC TAT TTC ACG CAC CGA ATC CGG CAA AAC GGA ATG GAA TGG TTT E G F V V D Y F T H R I R Q N G M E W F	100
BH4	
GGA GCA CCG GGA TTG CCG TGT GGA GTG CAA CCG GAG CAC GAA ATG G A P G L P C G V Q P E H E M M R V M G	120
ACG ATA TTC GAG AAG AAG CAC GCG GAA AAT TTT GAG ACC TTC TGT GAG CAG CTG CTC GCA T I F E K K H A E N F E T F C E Q L L A	140
GTG CCC AGA ATC TCA TTT TCA CTG TAT CAG GAT GTG GTT CGG ACG GTT GGA AAT GCA CAG V P R I S F S L Y Q D V V R T V G N A Q	160
ACA GAT CAA TGT CCA ATG TCT TAT GGA CGT TTG ATA GGT CTA ATC TCG TTC GGC GGT TTC T D Q C P M S Y G R L I G L I S F G G F	180
BH1	
GTA GCT GCA AAA ATG ATG GAA TCC GTG GAA CTG CAG GGA CAA GTG CGA AAC CTC TTC GTT V A A K M M E S V E L Q G Q V R N L F V	200
TAC ACA TCG CTG TTC ATC AAA ACG CGG ATC CGC AAC AAC TGG AAG GAA CAC AAT CGG AGC Y T S L F I K T R I R N N W K E H N R S	220
BH2	
TGG GAC GAC TTC ATG ACA CTC GGA AAA CAA ATG AAA GAG GAC TAC GAA GCA GAA GCT W D D F M T L G K Q M K E D Y E R A E A	240
GAA AAA GTG GGA CGC CGG AAG CAG AAC AGA CCG TGG TCG ATG ATT GGC GCT GGA GTA ACA E K V G R R K Q N R R W S M I G A G V T	260
GCT GGA GCC ATT GGA ATC GTT GGA GTC GTC GTG TGT GGG CGG ATG ATG TTC AGC TTG AAG A G A I G I V G V V C G R M M F S L K	280